

SEQUENCE LISTING

<110> TSURUOKA, Nobuo
YAMASHIRO, Kyoko
YAMAGUCHI, Nozomi

<120> Novel Serine Protease

<130> 001560-349

<140> US 09/147,947

<141> 1999-03-24

<150> PCT/JP98/03324

<151> 1998-07-24

<150> JP 9/213969

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<170> PatentIn Ver. 2.0

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:Synthetic DNA

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<222> (9)..(12)

<223> Nucleotides 9 and 12 are n wherein n = any nucleotide.

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<223> Description of Artificial Sequence:Synthetic DNA

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<223> Nucleotides 6 and 9 are n wherein n = any nucleotide.

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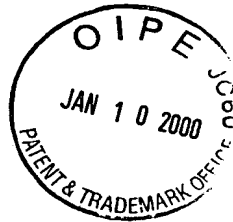
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60

120



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agcc atg gcg ctc gcc cgc tgc gtg ctg gct gtg att tta ggg gca ctg	289
Met Ala Leu Ala Arg Cys Val Leu Ala Val Ile Leu Gly Ala Leu	
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Ser Val Val Ala Arg Ala Asp Pro Val Ser Arg Ser Pro Leu His Arg	
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ccg cat ccg tcc cca ccg cgt tcc caa cac gcg cac tac ctt ccc agc	385
Pro His Pro Ser Pro Pro Arg Ser Gln His Ala His Tyr Leu Pro Ser	
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Ser Arg Arg Pro Pro Arg Thr Pro Arg Phe Pro Leu Pro Leu Arg Ile	
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Pro Ala Ala Gln Arg Pro Gln Val Leu Ser Thr Gly His Thr Pro Pro	
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Thr Ile Pro Arg Arg Cys Gly Ala Gly Glu Ser Trp Gly Asn Ala Thr	
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Tyr Pro Gly Gly Glu Gly His Arg Leu Ser Leu Gly Phe Pro Val Arg			
435 440 445			
ctg atg gat gga gaa aat aag aaa gaa gga cga gtg gag gtt ttt atc			1392
Leu Met Asp Gly Glu Asn Lys Lys Glu Gly Arg Val Glu Val Phe Ile			
450 455 460			
aat ggc cag tgg gga aca atc tgt gat gat gga tgg act gat aag gat			1440
Asn Gly Gln Trp Gly Thr Ile Cys Asp Asp Gly Trp Thr Asp Lys Asp			
465 470 475 480			
gca gct gtg atc tgt cgt cag ctt ggc tac aag ggt cct gcc aga gca			1488
Ala Ala Val Ile Cys Arg Gln Leu Gly Tyr Lys Gly Pro Ala Arg Ala			
485 490 495			
aga acc atg gct tac ttt gga gaa gga aaa gga ccc atc cat gtg gat			1536
Arg Thr Met Ala Tyr Phe Gly Glu Gly Lys Gly Pro Ile His Val Asp			
500 505 510			
aat gtg aag tgc aca gga aat gag agg tcc ttg gct gac tgt atc aag			1584
Asn Val Lys Cys Thr Gly Asn Glu Arg Ser Leu Ala Asp Cys Ile Lys			
515 520 525			
caa gat att gga aga cac aac tgc cgc cac agt gaa gat gca gga gtt			1632
Gln Asp Ile Gly Arg His Asn Cys Arg His Ser Glu Asp Ala Gly Val			
530 535 540			
att tgt gat tat ttt ggc aag aag gcc tca ggt aac agt aat aaa gag			1680
Ile Cys Asp Tyr Phe Gly Lys Lys Ala Ser Gly Asn Ser Asn Lys Glu			
545 550 555 560			
tcc ctc tca tct gtt tgt ggc ttg aga tta ctg cac cgt cgg cag aag			1728
Ser Leu Ser Ser Val Cys Gly Leu Arg Leu Leu His Arg Arg Gln Lys			
565 570 575			
cgg atc att ggt ggg aaa aat tct tta agg ggt ggt tgg cct tgg cag			1776
Arg Ile Ile Gly Gly Lys Asn Ser Leu Arg Gly Gly Trp Pro Trp Gln			
580 585 590			
gtt tcc ctc cgg ctg aag tca tcc cat gga gat ggc agg ctc ctc tgc			1824
Val Ser Leu Arg Leu Lys Ser Ser His Gly Asp Gly Arg Leu Leu Cys			
595 600 605			
ggg gct acg ctc ctg agt agc tgc tgg gtc ctc aca gca gca cac tgt			1872
Gly Ala Thr Leu Leu Ser Ser Cys Trp Val Leu Thr Ala Ala His Cys			
610 615 620			
ttc aag agg tat ggc aac agc act agg agc tat gct gtt agg gtt gga			1920
Phe Lys Arg Tyr Gly Asn Ser Thr Arg Ser Tyr Ala Val Arg Val Gly			

625	gat tat cat act ctg	630	gta cca gag gag ttt	635	gag gaa gaa att gga	640	ggt	1968
Asp Tyr His Thr	Leu Val Pro Glu Glu	Phe	Glu Glu Glu Ile	Gly	Val			
	645		650		655			
caa cag att gtg att	cat cgg gag tat	cga ccc gac cgc	agt gat tat	2016				
Gln Gln Ile Val Ile	His Arg Glu Tyr	Arg Pro Asp Arg	Ser Asp Tyr					
	660		665		670			
gac ata gcc ctg gtt	aga tta caa gga cca	gaa gag caa tgt	gcc aga	2064				
Asp Ile Ala Leu Val	Arg Leu Gln Gly	Pro Glu Glu Gln	Cys Ala Arg					
	675		680		685			
ttc agc agc cat gtt	ttg cca gcc tgt	tta cca ctc tgg	aga gag agg	2112				
Phe Ser Ser His Val	Leu Pro Ala Cys	Leu Pro Leu Trp	Arg Glu Arg					
	690		695		700			
cca cag aaa aca gca	tcc aac tgt tac	ata aca gga tgg	ggt gac aca	2160				
Pro Gln Lys Thr Ala	Ser Asn Cys Tyr	Ile Thr Gly Trp	Gly Asp Thr					
	705		710		715		720	
gga cga gcc tat tca	aga aca cta caa	caa gca gcc att	ccc tta ctt	2208				
Gly Arg Ala Tyr Ser	Arg Thr Leu Gln	Gln Ala Ala Ile	Pro Leu Leu					
	725		730		735			
cct aaa agg ttt tgt	gaa gaa cgt tat	aag ggt cgg ttt	aca ggg aga	2256				
Pro Lys Arg Phe Cys	Glu Glu Arg Tyr	Lys Gly Arg Phe	Thr Gly Arg					
	740		745		750			
atg ctt tgt gct gga	aac ctc cat gaa	cac aaa cgc gtg	gac agc tgc	2304				
Met Leu Cys Ala Gly	Asn Leu His Glu	His Lys Arg Val	Asp Ser Cys					
	755		760		765			
cag gga gac agc gga	gga cca ctc atg	tgt gaa cgg ccc	gga gag agc	2352				
Gln Gly Asp Ser Gly	Gly Pro Leu Met	Cys Glu Arg Pro	Gly Glu Ser					
	770		775		780			
tgg gtg gtg tat ggg	gtg acc tcc tgg	ggg tat ggc tgt	gga gtc aag	2400				
Trp Val Val Tyr Gly	Val Thr Ser Trp	Gly Tyr Gly Cys	Gly Val Lys					
	785		790		795		800	
gat tct cct ggt gtt	tat acc aaa gtc	tca gcc ttt gta	cct tgg ata	2448				
Asp Ser Pro Gly Val	Tyr Thr Lys Val	Ser Ala Phe Val	Pro Trp Ile					
	805		810		815			
aaa agt gtc acc aaa	ctg taattcttca	tggaacttc aaagcagcat		2496				
Lys Ser Val Thr Lys	Leu							
	820							
ttaaacaat ggaaaacttt	gaacccccac tattagcact	cagcagagat gacaacaaac		2556				
ggcaag				2562				

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Pro Thr Thr Arg Pro	Pro Pro Pro Pro	Leu Pro Arg Phe	Pro Arg Pro Pro
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Arg Ala Leu Pro Ala	Gln Arg Pro His	Ala Leu Gln Ala	Gly His Thr
	20	25	30
Pro Arg Pro His Pro	Trp Gly Cys Pro	Ala Gly Glu Pro	Trp Val Ser
	35	40	45
Val Thr Asp Phe Gly	Ala Pro Cys Leu	Arg Trp Ala Glu	Val Pro Pro
	50	55	60
Phe Leu Glu Arg Ser	Pro Pro Ala Ser	Trp Ala Gln Leu	Arg Gly Gln
	65	70	75
Arg His Asn Phe Cys	Arg Ser Pro Asp	Gly Ala Gly Arg	Pro Trp Cys
	85	90	95
Phe Tyr Gly Asp Ala	Arg Gly Lys Val	Asp Trp Gly Tyr	Cys Asp Cys
	100	105	110
Arg His Gly Ser Val	Arg Leu Arg Gly	Gly Lys Asn Glu	Phe Glu Gly
	115	120	125

Thr	Val	Glu	Val	Tyr	Ala	Ser	Gly	Val	Trp	Gly	Thr	Val	Cys	Ser	Ser
130						135					140				
His	Trp	Asp	Asp	Ser	Asp	Ala	Ser	Val	Ile	Cys	His	Gln	Leu	Gln	Leu
145					150					155					160
Gly	Gly	Lys	Gly	Ile	Ala	Lys	Gln	Thr	Pro	Phe	Ser	Gly	Leu	Gly	Leu
				165					170						175
Ile	Pro	Ile	Tyr	Trp	Ser	Asn	Val	Arg	Cys	Arg	Gly	Asp	Glu	Glu	Asn
			180					185					190		
Ile	Leu	Leu	Cys	Glu	Lys	Asp	Ile	Trp	Gln	Gly	Gly	Val	Cys	Pro	Gln
		195					200					205			
Lys	Met	Ala	Ala	Ala	Val	Thr	Cys	Ser	Phe	Ser	His	Gly	Pro	Thr	Phe
	210					215					220				
Pro	Ile	Ile	Arg	Leu	Ala	Gly	Gly	Ser	Ser	Val	His	Glu	Gly	Arg	Val
225					230					235					240
Glu	Leu	Tyr	His	Ala	Gly	Gln	Trp	Gly	Thr	Val	Cys	Asp	Asp	Gln	Trp
				245					250					255	
Asp	Asp	Ala	Asp	Ala	Glu	Val	Ile	Cys	Arg	Gln	Leu	Gly	Leu	Ser	Gly
		260						265					270		
Ile	Ala	Lys	Ala	Trp	His	Gln	Ala	Tyr	Phe	Gly	Glu	Gly	Ser	Gly	Pro
		275					280					285			
Val	Met	Leu	Asp	Glu	Val	Arg	Cys	Thr	Gly	Asn	Glu	Leu	Ser	Ile	Glu
	290					295					300				
Gln	Cys	Pro	Lys	Ser	Ser	Trp	Gly	Glu	His	Asn	Cys	Gly	His	Lys	Glu
305					310					315					320
Asp	Ala	Gly	Val	Ser	Cys	Thr	Pro	Leu	Thr	Asp	Gly	Val	Ile	Arg	Leu
				325					330					335	
Ala	Gly	Gly	Lys	Gly	Ser	His	Glu	Gly	Arg	Leu	Glu	Val	Tyr	Tyr	Arg
			340					345					350		
Gly	Gln	Trp	Gly	Thr	Val	Cys	Asp	Asp	Gly	Trp	Thr	Glu	Leu	Asn	Thr
		355					360					365			
Tyr	Val	Val	Cys	Arg	Gln	Leu	Gly	Phe	Lys	Tyr	Gly	Lys	Gln	Ala	Ser
	370					375					380				
Ala	Asn	His	Phe	Glu	Glu	Ser	Thr	Gly	Pro	Ile	Trp	Leu	Asp	Asp	Val
385					390					395					400
Ser	Cys	Ser	Gly	Lys	Glu	Thr	Arg	Phe	Leu	Gln	Cys	Ser	Arg	Arg	Gln
				405					410					415	
Trp	Gly	Arg	His	Asp	Cys	Ser	His	Arg	Glu	Asp	Val	Ser	Ile	Ala	Cys
			420					425					430		
Tyr	Pro	Gly	Gly	Glu	Gly	His	Arg	Leu	Ser	Leu	Gly	Phe	Pro	Val	Arg
		435					440					445			
Leu	Met	Asp	Gly	Glu	Asn	Lys	Lys	Glu	Gly	Arg	Val	Glu	Val	Phe	Ile
	450					455					460				
Asn	Gly	Gln	Trp	Gly	Thr	Ile	Cys	Asp	Asp	Gly	Trp	Thr	Asp	Lys	Asp
465					470					475					480
Ala	Ala	Val	Ile	Cys	Arg	Gln	Leu	Gly	Tyr	Lys	Gly	Pro	Ala	Arg	Ala
				485					490					495	
Arg	Thr	Met	Ala	Tyr	Phe	Gly	Glu	Gly	Lys	Gly	Pro	Ile	His	Val	Asp
			500					505					510		
Asn	Val	Lys	Cys	Thr	Gly	Asn	Glu	Arg	Ser	Leu	Ala	Asp	Cys	Ile	Lys
		515					520					525			
Gln	Asp	Ile	Gly	Arg	His	Asn	Cys	Arg	His	Ser	Glu	Asp	Ala	Gly	Val
	530					535					540				
Ile	Cys	Asp	Tyr	Phe	Gly	Lys	Lys	Ala	Ser	Gly	Asn	Ser	Asn	Lys	Glu
545					550					555					560
Ser	Leu	Ser	Ser	Val	Cys	Gly	Leu	Arg	Leu	Leu	His	Arg	Arg	Gln	Lys
				565					570					575	
Arg	Ile	Ile	Gly	Lys	Asn	Ser	Leu	Arg	Gly	Gly	Trp	Pro	Trp	Gln	
			580				585					590			
Val	Ser	Leu	Arg	Leu	Lys	Ser	Ser	His	Gly	Asp	Gly	Arg	Leu	Leu	Cys
		595					600					605			
Gly	Ala	Thr	Leu	Leu	Ser	Ser	Cys	Trp	Val	Leu	Thr	Ala	Ala	His	Cys
	610					615					620				
Phe	Lys	Arg	Tyr	Gly	Asn	Ser	Thr	Arg	Ser	Tyr	Ala	Val	Arg	Val	Gly

625 630 635 640
 Asp Tyr His Thr Leu Val Pro Glu Glu Phe Glu Glu Glu Ile Gly Val
 645 650 655
 Gln Gln Ile Val Ile His Arg Glu Tyr Arg Pro Asp Arg Ser Asp Tyr
 660 665 670
 Asp Ile Ala Leu Val Arg Leu Gln Gly Pro Glu Glu Gln Cys Ala Arg
 675 680 685
 Phe Ser Ser His Val Leu Pro Ala Cys Leu Pro Leu Trp Arg Glu Arg
 690 695 700
 Pro Gln Lys Thr Ala Ser Asn Cys Tyr Ile Thr Gly Trp Gly Asp Thr
 705 710 715 720
 Gly Arg Ala Tyr Ser Arg Thr Leu Gln Gln Ala Ala Ile Pro Leu Leu
 725 730 735
 Pro Lys Arg Phe Cys Glu Glu Arg Tyr Lys Gly Arg Phe Thr Gly Arg
 740 745 750
 Met Leu Cys Ala Gly Asn Leu His Glu His Lys Arg Val Asp Ser Cys
 755 760 765
 Gln Gly Asp Ser Gly Gly Pro Leu Met Cys Glu Arg Pro Gly Glu Ser
 770 775 780
 Trp Val Val Tyr Gly Val Thr Ser Trp Gly Tyr Gly Cys Gly Val Lys
 785 790 795 800
 Asp Ser Pro Gly Val Tyr Thr Lys Val Ser Ala Phe Val Pro Trp Ile
 805 810 815
 Lys Ser Val Thr Lys Leu
 820